

09/023,483

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<u>L17</u>	L16 and pcr	15	<u>L17</u>
<u>L16</u>	random primer\$1 and multiple nucleic acid\$1	15	<u>L16</u>
<u>L15</u>	L14 and multiple nucleic acid\$1	2	<u>L15</u>
<u>L14</u>	multiplex PCR and random primer\$1	29	<u>L14</u>
<u>L13</u>	L10 and multiple nucleic acid\$1	3	<u>L13</u>
<u>L12</u>	L11 and contaminat\$3	0	<u>L12</u>
<u>L11</u>	L10 and (multiple target\$1 or multiple nucleic acid\$1)	7	<u>L11</u>
<u>L10</u>	random primer\$1 near5 PCR	139	<u>L10</u>
<u>L9</u>	random primer\$1 and PCR	1807	<u>L9</u>
<u>L8</u>	random primer\$1	2200	<u>L8</u>
<u>L7</u>	random primer\$1 near5 (multiple target\$1 or multiplex\$2 target\$1)	0	<u>L7</u>
<u>L6</u>	L5 and (multiple near5 target\$1 or multiple near5 nucleic acid\$1)	5	<u>L6</u>
<u>L5</u>	random priming amplification	6	<u>L5</u>
<u>L4</u>	L3 and contaminat\$3	3	<u>L4</u>
<u>L3</u>	L2 and (target\$1 or nucleic acid species)	6	<u>L3</u>
<u>L2</u>	random primer\$1 near5 (multiple or multiplex\$2)	6	<u>L2</u>
<u>L1</u>	radom prirmer\$1 near5 multiple near5 (target\$1 or nucleic acid species)	0	<u>L1</u>

END OF SEARCH HISTORY

WEST

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Term:

L10 and (multiple target\$1 or multiple nucleic acid\$1)	▲
	▼

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Search Results - Record(s) 1 through 7 of 7 returned.

-
- ☐ 1. 6440668. 17 Aug 99; 27 Aug 02. Method of DNA shuffling with polynucleotides produced by blocking or interrupting a synthesis or amplification process. Short; Jay M.. 435/6; 435/196 435/69.1 435/91.1 435/91.2 530/300 530/350 536/23.1 536/24.3. C12Q001/68 C12P019/34 C07H021/02 C07H021/04 C07K014/00.
-
- ☐ 2. 6391592. 14 Dec 00; 21 May 02. Blocker-aided target amplification of nucleic acids. Su; Xing, et al. 435/91.1; 435/6 435/91.2. C12P019/34 C12Q001/68.
-
- ☐ 3. 6280949. 17 Sep 99; 28 Aug 01. Multiple displacement amplification. Lizardi; Paul M.. 435/6; 435/91.1 435/91.2 435/91.51 435/91.52 536/24.3. C12P019/34 C07H021/04.
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- ☐ 4. 6270971. 30 Jun 99; 07 Aug 01. Methods for detecting chromosomal aberrations using chromosome-specific paint probes. Ferguson-Smith; Malcolm A, et al. 435/6; 536/24.31. C12Q001/68 C07H021/04.
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- ☐ 5. 6255465. 27 Feb 98; 03 Jul 01. Cross-species chromosome painting. Ferguson-Smith; Malcolm A, et al. 536/23.1; 435/6 536/24.3 536/24.31. C07H021/02 C07H021/04 C12Q001/68.
-
- ☒ 6. 6124120. 08 Oct 97; 26 Sep 00. Multiple displacement amplification. Lizardi; Paul M.. 435/91.2; 435/91.1 435/91.52 536/22.1 536/24.33. C12P019/34 C07H021/04.
-
- ☐ 7. 5965408. 09 Jul 96; 12 Oct 99. Method of DNA reassembly by interrupting synthesis. Short; Jay M.. 435/91.1; 435/183 435/6 435/91.2 436/501 530/350 536/23.1 536/24.3 536/24.33. C12P019/34 C12N009/12 C07H021/04 G01N033/48.
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side by side			result set
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<u>L1</u>	radom primer\$1 near5 multiple near5 (target\$1 or nucleic acid species)	0	<u>L1</u>

END OF SEARCH HISTORY



Generate Collection

L11: Entry 6 of 7

File: USPT

Sep 26, 2000

DOCUMENT-IDENTIFIER: US 6124120 A

TITLE: Multiple displacement amplification

Brief Summary Text (5):

A variant of PCR amplification, termed whole genome PCR, involves the use of random or partially random primers to amplify the entire genome of an organism in the same PCR reaction. This technique relies on having a sufficient number of primers of random or partially random sequence such that pairs of primers will hybridize throughout the genomic DNA at moderate intervals. Replication initiated at the primers can then result in replicated strands overlapping sites where another primer can hybridize. By subjecting the genomic sample to multiple amplification cycles, the genomic sequences will be amplified. Whole genome PCR has the same disadvantages as other forms of PCR.

Detailed Description Text (5):

The target sequence, which is the object of amplification, can be any nucleic acid. The target sequence can include multiple nucleic acid molecules, such as in the case of whole genome amplification, multiple sites in a nucleic acid molecule, or a single region of a nucleic acid molecule. For multiple strand displacement amplification, generally the target sequence is a single region in a nucleic acid molecule or nucleic acid sample. For whole genome amplification, the target sequence is the entire genome or nucleic acid sample. A target sequence can be in any nucleic acid sample of interest. The source, identity, and preparation of many such nucleic acid samples are known. It is preferred that nucleic acid samples known or identified for use in amplification or detection methods be used for the method described herein. The nucleic acid sample can be a nucleic acid sample from a single cell. For multiple strand displacement amplification, preferred target sequences are those which are difficult to amplify using PCR due to, for example, length or composition. For whole genome amplification, preferred target sequences are nucleic acid samples from a single cell. For multiple strand displacement amplification of concatenated DNA the target is the concatenated DNA. The target sequences for use in the disclosed method are preferably part of nucleic acid molecules or samples that are complex and non-repetitive (with the exception of the linkers in linker-concatenated DNA and sections of repetitive DNA in genomic DNA).

End of Result Set

Generate Collection

L17: Entry 15 of 15

File: USPT

Aug 3, 1999

DOCUMENT-IDENTIFIER: US 5932451 A

TITLE: Method for unbiased mRNA amplification

Detailed Description Text (5):

The subject invention provides methods for producing amplified amounts of nucleic acid from an initial amount of mRNA. By amplified amounts is meant that for each initial mRNA, multiple corresponding nucleic acids, where the term nucleic acids is used broadly to refer to RNA and DNA, are produced. By corresponding is meant that the nucleic acid shares a substantial amount of sequence identity with the mRNA, the corresponding first strand cDNA or the second strand cDNA which can be prepared therefrom, where substantial amount means at least 95%, usually at least 98% and more usually at least 99%. Generally, the number of corresponding nucleic acids produced for each initial mRNA during amplification will be at least about 10, usually at least about 50 and more usually at least about 100.

Detailed Description Text (20):

For asymmetric amplification, the sense strand ss DNA is used as template in asymmetric amplification in at least one round of second primer extension product synthesis, where typically the sense strand DNA will be used in a plurality of rounds or cycles of primer extension product synthesis, where by plurality is meant at least 2, and usually at least 20, more usually at least 50 and typically at least 100 cycles. The primer extension products will be synthesized by the polymerase chain reaction in which only a single primer complementary to at least a portion of the 3' terminus of known but arbitrary sequence of the sense strand ss DNA is employed. The polymerase chain reaction (PCR), as well as devices and reagents for use in performing PCR, are described in U.S. Pat. Nos.: 4,683,202; 4,683,195; 4,800,159; 4,965,188 and 5,512,462, the disclosures of which are herein incorporated by reference. Of particular interest for performing this PCR step is the Rapidcycler sold by Idaho Technology Inc., Idaho Falls, Id.

Detailed Description Text (21):

The enzymatic extension is carried out in the presence of a DNA polymerase, dNTPs, and suitable buffering and other reagents necessary or desirable for optimal synthesis of primer extension product, as are known in the art. A variety of different polymerases are known and may be used in the synthesis of this first captureable primer extension product. Suitable polymerases include: E. coli DNA polymerase I (holoenzyme), Klenow fragment, T4 and T7 encoded polymerases, modified bacteriophage T7 DNA polymerase (Sequenase.TM.), as well as thermostable DNA polymerases, such as Taq DNA polymerase and AmpliTaq.TM.. Since thermal cycling is typically used in this portion of the method, a thermostable DNA polymerase is preferably employed for the synthesis of this second captureable primer extension product, where Taq DNA polymerase and AmpliTaq.TM. are representative of suitable thermostable polymerase. Buffers and other requisite reagents for performing PCR as described above are well known to those of skill in the art.

Detailed Description Text (38):

One way of producing cDNA from the resultant aRNA is to prime the aRNA with random primers, as described above, e.g. hexamers, under conditions sufficient to produce primer extension product. In some embodiments of the subject invention, of particular interest is the use of the subject methods to prepare cDNA probes for hybridization to chips.

Detailed Description Text (41):

Also provided are kits for use in the subject invention, where such kits may comprise

containers, each with one or more of the various reagents (typically in concentrated form) utilized in the methods, including, for example, buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP and dTTP; or rATP, rCTP, rGTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more primer complexes of the present invention (e.g., appropriate length poly(T) or random primers linked to a promoter reactive with the RNA polymerase). A set of instructions will also typically be included, where the instructions may associated with a package insert and/or the packaging of the kit or the components thereof.

Detailed Description Text (48):

Asymmetric amplification is performed by single biotinylated primer PCR (Biotin-CCTGGGCCCT CCTGCTCCTT) (SEQ ID NO:02) (Biotin-111-dCTP from NEN Life Science, Boston, Mass.) in the Rapidcycler.TM. PCR cyclor from Idaho Technology, Idaho Falls, Id., according to the manufacturers instructions using suggested reagent concentrations and volumes. Asymmetric amplification results in the production of multiple copies of first strand cDNA which are biotinylated at the 5' end.

Detailed Description Text (50):

80 .mu.l of streptavidin coated magnetic beads (Dynabeads M-280) are washed with 2.times.80 .mu.l binding and washing (B&W) buffer (10 mM Tris-HCl, pH 7.5, 1 mM EDTA and 2.0 M NaCl) and then resuspended in 50 .mu.l of B&W buffer. The entire PCR reaction mixture from Step B is combined with 50 .mu.l of the streptavidin coated magnetic beads (Dynal) and incubated at 37.degree. C. for one hour with occasional mixing. The supernatant is removed while the magnetic beads are immobilized with a magnet. The beads are then washed twice with 2.times.100 .mu.l of B&W buffer, once with 100 .mu.l 1.times.TE and once with 100 .mu.l of deionized water.

Detailed Description Text (66):

III. Demonstration of Linear Amplification by Assymetric PCR

Detailed Description Text (67):

A 2.3 kb control RNA (Gibco BRL) was converted to ds cDNA using the Superscript Choice System cDNA synthesis kit according to the manufacturer's instructions (Gibco BRL) and a Not1 primer (5'TTCTCGAGGCTAGCGAGCTCGCGCCGC(T)18VN) (SEQ ID NO: 05). The full length ds cDNA was gel purified over a 0.8% agarose gel with Geneclean glass beads (BIO101) and the concentration of purified DNA was determined by absorbance at 260 nm. The template as serially diluted to 55, 27.5 and 13.75 ng/.mu.l and 6 asymmetric PCR reactions for each template concentration were set up: 1.times.Amplitaq PCR buffer (Perkin Elmer), 100 .mu.g/ml BSA, 5 pmol Not2 primer (5'CTCGAGGCTAGCGAGCTC) (SEQ ID NO:06), 200 .mu.M dATP, 200 .mu.M dCTP, 200 .mu.M dTTP, 200 .mu.dGTP, 2.5 .mu.Ci .sup.32 P-dCTP (3000 Ci/mmol), 1 unit Amplitaq DNA polymerase (Perkin Elmer). Reactions were transferred to glass capillaries and were cycled in a Rapidcyclor PCR machine (Idaho Technology) at 94 for 0 sec, 58 for 3 sec, and 72 for 20 sec. the appropriate capillaries were removed at t=0, 25, 50, 75, 100 and 125 cycles. The amount of product synthesized was determined by adsorbing an aliquot from each reaction to DE-81 filters and washing with synthesized Na.sub.2 HPO.sub.4. A "no DNA" control prepared as above in parallel gave a calculated 5.6 ng for 125 cycles.

Other Reference Publication (2):

Barnard, Ross et al., "Two-Step PCR Amplification of Multiple Specific Products from cDNA Using One Specific Primer and Oligo dT," BioTechniques (1994) vol. 16 (2):251-252.